

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 14:20:50 ; Search time 18 Seconds
(without alignments)
1307.539 Million cell updates/sec

Title: US-09-787-678A-1

Perfect score: 2314

Sequence: 1 MAAALRSWCRCPRCLGS.....NPYAAWRLLDISASSTEQIL 452

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2314	100.0	452	1	IM44_HUMAN
2	212.5	91.3	453	1	IM44_RAT
3	2108	91.1	452	1	IM44_MOUSE
4	918.5	39.7	425	1	IM44_CABEL
5	441.5	19.1	427	1	IM44_SCHPO
6	406	17.5	431	1	IM44_YEAST
7	141	6.1	1093	1	TMF1_HUMAN
8	140.5	6.1	612	1	RPSD_BUCAL
9	140.5	6.1	879	1	RA50_PYRHO
10	139	6.0	978	1	RA50_AQUAE
11	137.5	5.9	3259	1	GOB1_HUMAN
12	134.5	5.8	658	1	VAT1_METTH
13	133.5	5.8	2116	1	MY52_DICDI
14	133	5.7	2663	1	CENE_HUMAN
15	132.5	5.7	808	1	Y066_NPVAC
16	132.5	5.7	1939	1	MYH1_HUMAN
17	132	5.7	1940	1	GAS8_HUMAN
18	132	5.7	1940	1	MYH3_RAT
19	131.5	5.7	1203	1	SMC2_XENLA
20	131.5	5.7	8797	1	SNE1_HUMAN
21	130.5	5.6	919	1	RA50_AERPE
22	130.5	5.6	1169	1	SMC_METJA
23	130	5.6	852	1	RA50_THEMA
24	130	5.6	2017	1	MY5N_DROME
25	129.5	5.6	1433	1	RSTN_CHICK
26	129.5	5.6	1957	1	SPOF_SCHPO
27	129	5.6	1938	1	MYHD_HUMAN
28	128.5	5.6	1114	1	RH18_YEAST
29	128	5.5	851	1	YD72_SCHPO
30	127.5	5.5	520	1	REC7_AQUAE
31	127.5	5.5	1288	1	SMC4_HUMAN
32	127	5.5	1182	1	CGA2_HELPY
33	127	5.5	1940	1	MYH3_HUMAN

34	127	5.5	2867	1	RBP2_PLAIVB
35	126.5	5.5	1940	1	MYH3_CHICK
36	126	5.4	1163	1	SBCC_CLOAB
37	125.5	5.4	1790	1	USO1_YEAST
38	125	5.4	811	1	HSP7_YEAST
39	125	5.4	2230	1	GOA4_HUMAN
40	125	5.4	4687	1	PLE1_RAT
41	124.5	5.4	1938	1	MYSS_CHICK
42	124.5	5.4	1939	1	MYH4_HUMAN
43	124	5.4	541	1	EH44_MOUSE
44	124	5.4	875	1	ZIP1_YEAST
45	124	5.4	1046	1	SBCC_LACLA

ALIGNMENTS

RESULT 1
IM44_HUMAN
ID IM44_HUMAN STANDARD; PRT; 452 AA.
AC O43615; Q8N193;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Import inner membrane translocase subunit TIM44, mitochondrial precursor.
DE TIM44 OR MIMT44 OR TIM44.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=92272555; PubMed=10339406;
RA Bauer M.F., Gempel K., Reichert A.S., Rappold G.A., Lichtner P., Gerbitz K.D., Neupert W., Brunner M., Hofmann S.;
RT "Genetic and structural characterization of the human mitochondrial inner membrane translocase".
RL J. Mol. Biol. 289:69-82(1999). MAY
[2]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butler A.Y., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in protein import into the mitochondrion. Probably involved in translocation across the inner membrane. As a binding protein required for driving the import of preproteins. Recruits mitochondrial HSP70 to drive protein translocation into the matrix using ATP as an energy source.
CC -!- SUBUNIT: Forms part of the receptor complex that consists of at least 3 different proteins (TIM17, TIM23, TIM44) (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the Tim44 family.

Q00799	plasmodium
P02565	gallus gall
Q97fki	clostridium
P25386	saccharomyc
P33416	saccharomyc
Q13439	homo sapien
P30427	rattus norv
P13538	gallus gall
Q95623	homo sapien
Q9eqp2	mus musculu
P31111	saccharomyc
Q9cfz0	lactococcus

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DE EMBL; AF041254; AAH97740.1; --
 DE EMBL; BC033628; AAB33628.1; --
 GN Genev; HGNC:17316; TIMM44.
 DR MM: 605058; --
 DR GO: GO:0005759; C-mitochondrial matrix; TAS.
 DR GO: GO:0006628; P-mitochondrial translocation; TAS.
 DR InterPro; IPR007379; Tim44.
 DR InterPro; IPR005682; Tim44_sub.
 DR Pfam; PF04280; Tim44; 1.
 DR TIGRFAMs; TIGR00984; 3a0801s03tim44; 1.
 KW Mitochondrion; Inner membrane; Transport; Protein transport;
 KW Translocation; Transmembrane; Transmembrane; ATP-binding;
 FT TRANSIT ?
 FT CHAIN 1 452
 FT IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT
 FT TIM44.
 FT NP_BIND 166 173
 FT CONFLICT 189 189
 FT CONFLICT 226 226
 FT SEQUENCE 452 AA; 51355 MW; 15BECF875611BE96 CRC64;

Query Match 100.0%; Score 2314; DB 1; Length 452;
 Best Local Similarity 100.0%; Pred. No. 1.1e-117;
 Matches 452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPPGGELPLSKSYSSGNRGFL 60
 DB 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPPGGELPLSKSYSSGNRGFL 60
 QY 61 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKTTIESEVLRK 120
 DB 61 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKTTIESEVLRK 120
 QY 121 KLGLTGTVKESLHEVSKSDLGRIKKEGVAAAKTAKQSAESVSKGEGKLGRTAAPRAL 180
 DB 121 KLGLTGTVKESLHEVSKSDLGRIKKEGVAAAKTAKQSAESVSKGEGKLGRTAAPRAL 180
 QY 181 QGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEALGVVLHKDSK 240
 DB 181 QGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEALGVVLHKDSK 240
 QY 241 WYQWKDFKNNVFNFRFFEMKKYDESDNAFTASRALTDKVTDLGLFSKTEMSEVL 300
 DB 241 WYQWKDFKNNVFNFRFFEMKKYDESDNAFTASRALTDKVTDLGLFSKTEMSEVL 300
 QY 301 TEILRVDPAPDKDRFLKQCENDIIPNVLEAMISGELDLKWCYEATYSQLAHPITQAKA 360
 DB 301 TEILRVDPAPDKDRFLKQCENDIIPNVLEAMISGELDLKWCYEATYSQLAHPITQAKA 360
 QY 361 LGLQPHSRILDDNVDLAMGKWEQGVLIITFQALVWVRNPKGEVVEGDPDKVLRML 420
 DB 361 LGLQPHSRILDDNVDLAMGKWEQGVLIITFQALVWVRNPKGEVVEGDPDKVLRML 420
 QY 421 YWALCRDQDELNPYAANRLDIDISASSTEQIL 452
 DB 421 YWALCRDQDELNPYAANRLDIDISASSTEQIL 452

RESULT 2
 ID IM44 RAT
 AC O35094
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Import inner membrane translocase subunit TIM44, mitochondrial
 DE precursor.
 GN TIMM44 OR TIMM44 OR TIM44.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98207064; PubMed=9538267;
 RA Ishihara N., Mihara K.;
 RT Identification of the protein import components of the rat
 RT mitochondrial inner membrane, rTIM17, rTIM23, and rTIM44.";
 RL J. Biochem. 123:722-732(1998).
 CC -!- FUNCTION: Involved in protein import into the mitochondrion.
 CC Probably involved in translocation across the inner membrane. As a
 CC binding protein required for driving the import of preproteins.
 CC Recruits mitochondrial HSP70 to drive protein translocation into
 CC the matrix using ATP as an energy source.
 CC -!- SUBUNIT: Forms part of the receptor complex that consists of at
 CC least 3 different proteins (TIM17, TIM23, TIM44) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the Tim44 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DE EMBL; AB006452; BAA21820.1; --
 DE PIR; JE0155; JE0155.
 DR InterPro; IPR007379; Tim44.
 DR InterPro; IPR005682; Tim44_sub.
 DR Pfam; PF04280; Tim44; 1.
 DR TIGRFAMs; TIGR00984; 3a0801s03tim44; 1.
 KW Mitochondrion; Inner membrane; Transport; Protein transport;
 KW Translocation; Transmembrane; Transmembrane; ATP-binding;
 FT TRANSIT ?
 FT CHAIN 1 453
 FT IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT
 FT TIM44.
 FT NP_BIND 167 174
 FT SEQUENCE 453 AA; 51060 MW; 387C85147C577A0 CRC64;

Query Match 91.3%; Score 2112.5; DB 1; Length 453;
 Best Local Similarity 90.1%; Pred. No. 7.6e-107;
 Matches 408; Conservative 24; Mismatches 20; Indels 1; Gaps 1;

QY 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPPGGELPLSKSYSSGNRGFL 59
 DB 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPPGGELPLSKSYSSGNRGFL 60
 QY 60 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKTTIESEVLRK 119
 DB 61 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKTTIESEVLRK 120
 QY 120 KLGLTGTVKESLHEVSKSDLGRIKKEGVAAAKTAKQSAESVSKGEGKLGRTAAPRAL 179
 DB 121 KLGLTGTVKESLHEVSKSDLGRIKKEGVAAAKTAKQSAESVSKGEGKLGRTAAPRAL 180
 QY 180 QGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEALGVVLHKDS 239
 DB 181 QGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEALGVVLHKDS 240
 QY 240 WYQWKDFKNNVFNFRFFEMKKYDESDNAFTASRALTDKVTDLGLFSKTEMSEVL 299
 DB 241 WYQWKDFKNNVFNFRFFEMKKYDESDNAFTASRALTDKVTDLGLFSKTEMSEVL 300
 QY 300 TEILRVDPAPDKDRFLKQCENDIIPNVLEAMISGELDLKWCYEATYSQLAHPITQAK 359